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Msrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Sat May 13 09:29:15 2000; Maspar time 3.98 seconds  
Tabular output not generated. 267.936 Million cell updates/sec

Title: >US-09-331-631-1  
Description: (29-73) from US09331631.pap (2 of 5)  
Perfect score: 361  
Sequence: 1 SEFDROEYECRCQCMQLETSQMRRCVSCQDKRFEDIDMSKYD 45

Scoring table:  
PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a:geneseq35  
1:geneseqp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	361	100.0	666	1 W62829	Macadamia integrifolia	2.58e-30
2	361	100.0	666	1 W62828	Macadamia integrifolia	2.58e-30
3	259	71.7	625	1 W62830	Macadamia integrifolia	9.96e-19
4	109	30.2	590	1 W62832	Gossypium hirsutum ant	1.26e-02
5	97	26.9	525	1 W62831	Theobroma cacao anti	1.88e-01
6	97	26.9	566	1 R20181	Sequence encoded by 67	1.88e-01
7	95	26.3	218	1 W40287	Human rspl protein.	2.93e-01
8	95	26.3	239	1 R40823	Human thrombospondin 1	2.93e-01
9	95	26.3	441	1 W40288	Human concanamersin T	2.93e-01
10	77	21.3	62	1 W03698	Maize id gene product.	1.33e+01
11	77	21.3	409	1 W90342	G. max truncated SBP2	1.33e+01
12	77	21.3	438	1 W59836	G. max truncated SBP2	1.33e+01
13	77	21.3	444	1 W90340	G. max truncated SBP1	1.33e+01
14	77	21.3	489	1 W90341	G. max truncated SBP1	1.33e+01
15	77	21.3	524	1 W90339	G. max SBP1 protein.	1.33e+01
16	77	20.2	81	1 Y12435	Human 5' EST secreted	3.18e+01
17	73	20.2	125	1 R13329	Human 5' EST secreted	3.18e+01
18	73	20.2	125	1 W81779	Human H54 protein.	3.18e+01
19	73	20.2	1284	1 P81187	Sequence encoded by a	3.18e+01
20	72	19.9	593	1 W62835	Zea mays antimicrobial	3.90e+01
21	72	19.9	1416	1 R67358	Human astrovirus serot	3.90e+01
22	71	19.7	2703	1 R70236	P. falciparum Pfoj3.	4.77e+01
23	71	19.7	2710	1 W22482	Plasmodium Pfoj3.	4.77e+01

24	71	19.7	3060	1 W22475	Plasmodium var-7.	4.77e+01
25	70	19.4	103	1 Y11721	Human 5' EST secreted	5.83e+01
26	70	19.4	191	1 R91311	N. gonorrhoeae glycosyl	5.83e+01
27	70	19.4	348	1 W06576	Neisseria polysacchari	5.83e+01
28	69	19.1	348	1 W62836	Zea mays antimicrobial	7.13e+01
29	69	19.1	35	1 R21079	Antimicrobial maize pe	7.13e+01
30	68	18.8	623	1 W30622	Arabidopsis enhanced p	8.70e+01
31	68	18.8	816	1 R85870	WD-40 domain-contg. Mu	8.70e+01
32	68	18.8	1479	1 W44119	Human type C lectin.	8.70e+01
33	67	18.6	203	1 Y04837	Mycobacterium species	1.06e+02
34	67	18.6	363	1 R47557	ILTV thymidine kinase.	1.06e+02
35	67	18.6	506	1 Y04841	Mycobacterium species	1.06e+02
36	67	18.6	974	1 W55960	Human transient recept	1.06e+02
37	66	18.3	30	1 W08904	(Cyclo 30-33)ID-Phe12,	1.29e+02
38	66	18.3	38	1 W07823	Cyclic corticotrophin	1.29e+02
39	66	18.3	194	1 R57061	P. aeruginosa muc.	1.29e+02
40	66	18.3	370	1 W54097	Homo sapiens B223 sequ	1.29e+02
41	66	18.3	676	1 R81473	Thermus aquaticus DNA	1.29e+02
42	66	18.3	676	1 W80302	A thermophilic ligase	1.29e+02
43	66	18.3	680	1 R15299	Thermotable T. aquati	1.29e+02
44	66	18.3	1496	1 Y04136	Human slit 3 mature pr	1.29e+02
45	66	18.3	1523	1 Y04137	Human slit 3 protein.	1.29e+02

## ALIGNMENTS

RESULT 1	ALIGNMENTS
ID W62829 standard; Protein; 666 AA.	
AC W62829 (first entry)	
DT 27-0CT-1998	
DE Macadamia integrifolia antimicrobial protein.	
KW antimicrobial protein; infestation; control.	
OS Macadamia integrifolia.	
FH key	location/Qualifiers
FT Peptide	1..28
FT Protein	/note="signal peptide"
FT	29..666
FT	/note="mature protein"
PN W09827805-A1.	
PD 02-JUL-1998	
PR 22-DEC-1997; AU0874	
PA (R2TR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;	
DR WPI: 98-377279/32.	
DR N-PSDB: V42311	
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -	
PT useful for controlling microbial infestations of plants or mammals	
PS Claim 1; Page 39-41; 96pp; English.	
CC The sequence is that of an antimicrobial protein which can	
CC be used to control microbial infestations in plants and mammalian	
CC animals.	
CC Sequence 666 AA;	
SO	
Query Match 100.0%; Score 361; DB 1; Length 666;	
Best Local Similarity 100.0%; Pred. No. 2.58e-30;	
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db 29 SEFDROEYECRCQCMQLETSQMRRCVSCQDKRFEDIDMSKYD 73	
Oy 29 SEFDROEYECRCQCMQLETSQMRRCVSCQDKRFEDIDMSKYD 73	
RESULT 2	
ID W62828 standard; Protein; 666 AA.	
AC W62828 (first entry)	
DT 27-0CT-1998	
DE Macadamia integrifolia antimicrobial protein.	
KW antimicrobial protein; infestation; control.	
OS Macadamia integrifolia.	
FH key	location/Qualifiers
FT Peptide	1..28
FT	/note="signal peptide"

FT Protein 29.666  
/note="mature protein"  
PN WO9827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997: AU0874.  
PR 20-DEC-1996: AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI: 98-377279/32.  
DR N-PSDB: V42310.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PS Claim 1; Page 34-36; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 666 AA;  
Query Match 100.0%; Score 361; DB 1; Length 666;  
Best Local Similarity 100.0%; Pred. No. 2.58e-30;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 29 SEFDRQYECKRCQMOLETSGMRRCVSCDCKRFEEDIDMSKYD 73  
QY 29 SEFDRQYECKRCQMOLETSGMRRCVSCDCKRFEEDIDMSKYD 73  
RESULT 3  
ID W62830 standard; Protein; 625 AA.  
AC W62830;  
DT 27-OCT-1998 (first entry)  
DE Macadamia integrifolia antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Macadamia integrifolia.  
FH Key location/Qualifiers  
FT Peptide 1..28  
/note="signal peptide"  
FT Protein 29..666  
/note="mature protein"  
FN WO9827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997: AU0874.  
PR 20-DEC-1996: AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI: 98-377279/32.  
DR N-PSDB: V42316.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PS Claim 1; Page 43-45; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 625 AA;  
Query Match 71.7%; Score 259; DB 1; Length 625;  
Best Local Similarity 100.0%; Pred. No. 9.96e-19;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 QCMOLETSGMRRCVSCDCKRFEEDIDMSKYD 32  
QY 42 QCMOLETSGMRRCVSCDCKRFEEDIDMSKYD 73  
RESULT 4  
ID W62832 standard; Protein; 590 AA.  
AC W62832;  
DT 27-OCT-1998 (first entry)  
DE Gossypium hirsutum antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Gossypium hirsutum.  
PN WO9827805-A1.  
PD 02-JUL-1998.

PF 22-DEC-1997: AU0874.  
PR 20-DEC-1996: AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI: 98-377279/32.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PS Claim 1; Page 49-51; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 590 AA;  
Query Match 30.2%; Score 109; DB 1; Length 590;  
Best Local Similarity 45.2%; Pred. No. 1.26e-02;  
Matches 14; Conservative 6; Mismatches 10; Indels 1; Gaps 1;  
Db 87 YEEQGCRCRQGER-QPQCQRCRKFEED 116  
QY 36 YEECKRCQMOLETSGMRRCVSCDCKRFEED 66  
RESULT 5  
ID W62831 standard; Protein; 525 AA.  
AC W62831;  
DT 27-OCT-1998 (first entry)  
DE Theobroma cacao antimicrobial protein.  
KW antimicrobial protein; infestation; control.  
OS Theobroma cacao.  
PN WO9827805-A1.  
PD 02-JUL-1998.  
PE 22-DEC-1997: AU0874.  
PR 20-DEC-1996: AU-004275.  
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.  
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;  
DR WPI: 98-377279/32.  
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -  
PS Claim 1; Page 47-49; 96pp; English.  
CC The sequence is that of an antimicrobial protein which can  
CC be used to control microbial infestations in plants and mammalian  
CC animals.  
SQ Sequence 525 AA;  
Query Match 26.9%; Score 97; DB 1; Length 525;  
Best Local Similarity 31.4%; Pred. No. 1.88e-01;  
Matches 11; Conservative 11; Mismatches 12; Indels 1; Gaps 1;  
Db 39 ROQYEQRCRCSEATEERQEQRCERERKEQ 73  
QY 33 ROYEECKRCQMOLETSGMR-RCVSCDCKRFEED 66  
RESULT 6  
ID R20181 standard; Protein; 566 AA.  
AC R20181;  
DT 16-APR-1992 (first entry)  
DE Sequence encoded by 67 kD T. cacao protein cDNA.  
KW Cocoa; flavour; vicillin; seed storage protein.  
OS Theobroma cacao.  
PN WO9119801-A.  
PD 26-DEC-1991.  
PE 07-JUN-1991: G00914.  
PR 11-JUN-1990: GB-013016.  
PA (MRSC) MARS UK LTD.  
PI Spencer ME, Hodge R, Deakin EA, Ashton S;  
DR WPI: 92-024418/03.  
DR N-PSDB: Q20377.  
PT Recombinant cocoa proteins - are responsible for flavour in cocoa  
PT beans and produced in large quantities using yeast and bacterial  
PT expression vectors  
PS Claim 4; Fig 2; 59pp; English.  
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and



Db 116 SSVQTRTCHIDCKRFRKDGGS 139  
 :| | | :| | | | | :| | |  
 OY 48 TSGMRRC-VSQCKRFEEDIDW 70

RESULT 10  
 ID W03698 standard; Protein: 62 AA.

AC W03698;  
 DT 06-MAR-1997 (first entry)  
 DE Maize Id gene product.  
 KW Maize: Zea mays; Id: id\*; transposon: transposable element;  
 KM Ds2; flower evocation; zinc-finger regulatory protein.

OS Zea mays.  
 PN W09634088-A2.  
 PD 31-OCT-1996.  
 PF 15-MAR-1996; U03466.  
 PZ 15-MAR-1995; US-406186.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PI Colasanti JJ, Sundaresan V;  
 DR WPI: 96-497621/49.  
 DR N-PSDB: T42174, T42175.

PT New isolated plant Id gene - used to develop prods. for use in altering the induction of flowering in plants  
 PS Claim 7, Fig 3 and Fig 5; 58pp; English.  
 CC The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-finger regulatory proteins in animals.  
 CC Transposons Ac and Ds constitute a family of related transposable elements present in maize. A derivative of Ds, Ds2, can be used to produce a new mutant of the Id gene. The Ds2 (in the presence of active Ac) is excised into a nearby gene on chromosome 1 and inserted into the Id gene to produce id\*.  
 SO Sequence 62 AA;

Query Match 21.3%; Score 77; DB 1; Length 62;  
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;  
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 17 GKRWCRCRCKPYAVOSDW 36  
 :| | | :| | | :| | |  
 OY 50 GMRRCVSCQCKRFEEDIDW 69

RESULT 11  
 ID W90342 standard; Protein: 409 AA.

AC W90342;  
 DT 24-MAY-1999 (first entry)  
 DE G. max truncated SBP2 protein.  
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 KM seed; carbohydrate content; soybean.  
 OS Glycine max.  
 PN W09853086-A1.  
 PD 26-NOV-1998.  
 PE 21-MAY-1998; U10465.  
 PF 22-MAY-1997; US-047568.  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;  
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds  
 PT uptake activity in developing seeds  
 PS Claim 7; Page 39-40; 58pp; English.  
 CC This sequence represents a novel SBP2 protein. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content

CC of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in CC seeds might be desirable where the vegetative material of the plant is CC harvested. The SBP regulatory regions confer specific or enhanced CC expression in developing seeds and so may be used to express any CC transgene in developing seeds.  
 SO Sequence 409 AA;

Query Match 21.3%; Score 77; DB 1; Length 409;  
 Best Local Similarity 45.8%; Pred. No. 1.39e+01;  
 Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 2;

Db 42 CKHCCQOQOYTESDKRCLQCCD 65  
 :| | | :| | | :| | |  
 OY 39 CKRCQMOLE-TSGMRRCVSCQCD 60

RESULT 12  
 ID W59836 standard; Protein: 438 AA.

AC W59836;  
 DT 16-NOV-1998 (first entry)  
 DE Maize Id protein.  
 KW Maize; Id: floral induction; transgenic plant.

OS Zea mays.  
 PN W09837201-A1.  
 PD 27-AUG-1998.  
 PF 18-FEB-1998; U03161.  
 PR 30-DEC-1997; US-000640.  
 PA 20-FEB-1997; US-804104.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PI Colasanti JJ, Sundaresan V;  
 DR WPI: 98-467564/40.  
 DR N-PSDB: V41721.

PT Id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops  
 PS Claim 5, Fig 3; 68pp; English.  
 CC The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc-finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity in CC plants.  
 SO Sequence 438 AA;

Query Match 21.3%; Score 77; DB 1; Length 438;  
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;  
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 187 GKRWCRCRCKPYAVOSDW 206  
 :| | | :| | | :| | |  
 OY 50 GMRRCVSCQCKRFEEDIDW 69

RESULT 13  
 ID W90340 standard; Protein: 444 AA.

AC W90340;  
 DT 24-MAY-1999 (first entry)  
 DE G. max truncated SBP1 protein.  
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 KM seed; carbohydrate content; soybean.  
 OS Glycine max.  
 PN W09853086-A1.  
 PD 26-NOV-1998.  
 PE 21-MAY-1998; U10465.  
 PF 22-MAY-1997; US-047568.  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD;  
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

PS Claim 7 Page 36-37: 58bp: English.  
CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
CC from Glycine max. This protein is used in a method resulting in the  
CC production of a modified plant sucrose binding protein (SBP) which has a  
CC modified amino acid sequence compared to a corresponding wild-type SBP,  
CC and where expression of the modified SBP in a yeast assay system confers  
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
CC The products of the invention can be used for producing transgenic plants  
CC which have modified sucrose uptake activity, particularly in developing  
CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
CC desirable where it is an advantage to increase the carbohydrate content  
CC of the seed (e.g. where the seed is the primary plant material harvested,  
CC such as soybean). In contrast, decreased sucrose uptake activity in  
CC seeds might be desirable where the vegetative material of the plant is  
CC harvested. The SBP regulatory regions confer specific or enhanced  
CC expression in developing seeds and so may be used to express any  
CC transgene in developing seeds.  
QQ Sequence 444 AA:

Query Match	21.38;	Score 77;	DB 1;	Length 444;
Best Local Similarity	44.48;	Pred. No. 1.39e+01;		
Matches	12;	Conservative	6;	Mismatches 6;
			Indels 3;	Gaps 2

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Db      43  CKHQCCQQQYTEGDKRVCLQSCD-RY 68
          ||:| | : | : | | : | | :
QY     39  CKRQCMQL E - TSGQMRRCVSGCDKRF 63

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RESULT 14  
 ID W90341 standard; protein; 489 AA.  
 DT W90341;  
 24-MAY-1999 (first entry)  
 DE G. max SBP2 protein.  
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 KW seed; carbohydrate content; soybean.  
 OS Glycine max.  
 PN W09853086-A1.  
 PD 26-NOV-1998.  
 PF 21-MAY-1998; U10465.  
 PR 22-MAY-1997; US-047568.  
 PA (UNITW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD:  
 DR WPT: 99-070155/06.  
 PT New modified plant sucrose binding proteins - used to develop  
 PT transgenic plants which can have enhanced or decreased sucrose  
 PT uptake activity in developing seeds  
 PS Claim 13b; Page 37-38; 58pp; English.  
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated  
 CC from Glycine max. This protein is used in a method resulting in the  
 CC production of a modified plant sucrose binding protein (SBP) which has a  
 CC modified amino acid sequence compared to a corresponding wild-type SBP,  
 CC and where expression of the modified SBP in a yeast assay system confers  
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
 CC The products of the invention can be used for producing transgenic plants  
 CC which have modified sucrose uptake activity, particularly in developing  
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
 CC desirable where it is an advantage to increase the carbohydrate content  
 CC of the seed (e.g. where the seed is the primary plant material harvested,  
 CC such as soybean). In contrast, decreased sucrose uptake activity in  
 CC seeds might be desirable where the vegetative material of the plant is  
 CC harvested. The SBP regulatory regions confer specific or enhanced  
 CC expression in developing seeds and so may be used to express any  
 CC transgene in developing seeds.  
 CC Sequence 489 AA:

Query Match	21.3%;	Score 77;	DB 1;	Length 489;
Best Local Similarity	45.8%;	Pred. No. 1.39e+01;		
Matches	11;	Conservative	6;	Mismatches 5; Indels 2; Gaps 2

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Db      42 CKHQCCQQRRQYTESDKRTCLQQCD 65
      11::111 : ::::111:111
QY     39 CKRQCMQL-E-TSGQMRRCVSSQCD 60
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RESULT 15  
 ID M90339 standard; protein; 524 AA.  
 AC M90339;  
 DT 24-MAY-1999 (first entry)  
 DE G. max SBP1 protein.  
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;  
 seed; carbohydrate content; soybean.  
 OS Glycine max.  
 PN M08853086-A1.  
 PD 26-NOV-1998.  
 PR 21-MAY-1998; U10465.  
 PR 22-MAY-1997; US-047568.  
 PA (UNITW ) UNIV WASHINGTON STATE RES FOUND.  
 PI Chao WS, Grimes HD:  
 DR WPI; 99-070155/06.  
 FT New modified plant sucrose binding proteins - used to develop  
 FT transgenic plants which can have enhanced or decreased sucrose  
 FT uptake activity in developing seeds  
 PS Disclosure; Page 34-36; 58pp; English.  
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated  
 CC from Glycine max. This protein is used in a method resulting in the  
 CC production of a modified plant sucrose binding protein (SBP) which has a  
 CC modified amino acid sequence compared to a corresponding wild-type SBP,  
 CC and where expression of the modified SBP in a yeast assay system confers  
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.  
 CC The products of the invention can be used for producing transgenic plants  
 CC which have modified sucrose uptake activity, particularly in developing  
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be  
 CC desirable where it is an advantage to increase the carbohydrate content  
 CC of the seed (e.g. where the seed is the primary plant material harvested,  
 CC such as soybean). In contrast, decreased sucrose uptake activity in  
 CC seeds might be desirable where the vegetative material of the plant is  
 CC harvested. The SBP regulatory regions confer specific or enhanced  
 CC expression in developing seeds and so may be used to express any  
 CC transgene in developing seeds.  
 Q0 Sequence 524 AA;

Query Match	21.3%;	Score 77;	DB 1;	Length 524;
Best Local Similarity	44.4%;	Pred. No. 1.39e+01;		
Matches	12;	Conservative	6;	Mismatches 6;
			Indels	3;
			Gaps	2;

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Db      43 CKHQCCQQQYTEGDKRVCLQSCD-RY 68
      11:111:111:111:
QY      39 CKRQCMGLE--TSGQMRRCVSGCDKRF 63

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Search completed: Sat May 13 09:29:23 2000  
Job time : 8 secs.

